



SEQUENCE LISTING

<110> Duvick, Jonathan P.
Gilliam, Jacob T.
Maddox, Joyce R.
Rao, Aragula Gururaj
Crasta, Oswald R.
Folkerts, Otto

<120> Amino Polyol Amine Oxidase
Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134R

<150> US 60/092,936
<151> 1998-07-25

<150> US 60/135,391
<151> 1999-05-21

<150> US 09/352,159
<151> 1999-07-12

<150> US 09/352,168
<151> 1999-07-12

<160> 53

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 372
<212> DNA
<213> *Exophiala spinifera*

<220>
<221> misc_feature
<222> (346)...(346)
<223> n = A,T,C or G

<400> 1

gggccccggc gttctcgtag gctgcgcgga gttgggtccca gacagaacttt tgctgtacct	60
gcttggaactg ttgggaccac ttccgtcccg ggtctccgac catgaaacag gtaatggacc	120
attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatggggtea cagctcgatt	180
ggaggacgac cgagaagcct tgttcgcgac accacggctt gtcccatacg aagactatct	240
tgctatagta gccacggata gaattttccg caaatgcttg cttctcggcg ggaagaggtg	300
gtgaaaatgt caaggtggga tacaaggttg tggtaacga aaccacacc ttttgcctc	360
ggaacacggc gc	372

<210> 2
<211> 182
<212> DNA
<213> *Exophiala spinifera*

<400> 2

gaattttccg caaatgcttg cttctcggcg ggaagaggtg gtgaaaatgt caaggtggga	60
---	----

tacaagggttg tgggtaacga aaccaccacc tttttgcttc ggaacacggc gcccgaggcc	120
gacgtactg tacagccgga tgccgactgc tcaatttcag cgacgggggt gttgaggtgc	180
ac	182

<210> 3
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 3' RACE, N21965

<400> 3	
tggttttcgta accgacaacc ttgtatccc	29

<210> 4
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 5' RACE, 21968

<400> 4	
gagttggtaa cagacagact tttgtcgt	28

<210> 5
 <211> 1389
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> CDS
 <222> (1)...(1386)

<400> 5	
gac aac gtt ggc gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg	48
Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu	
1 5 10 15	

gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt	96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	

ccc ggc agc acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
---	-----

Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp		
				85					90						95		
ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	gag	336	
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu		
			100					105					110				
gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	384	
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile		
		115					120					125					
gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	egg	432	
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg		
	130					135				140							
ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	480	
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu		
145					150				155					160			
cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt	528	
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly		
				165				170					175				
gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	576	
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys		
			180					185					190				
agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	624	
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly		
		195				200					205						
cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	atg	672	
Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met		
	210					215					220						
tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	720	
Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala		
225					230					235				240			
gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	768	
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly		
			245					250					255				
gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	816	
Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu		
			260					265				270					
tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	864	
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala		
		275				280					285						
ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	912	
Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val		
	290					295				300							
tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	960	
Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln		
305					310				315					320			

tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc	1008
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val	
325 330 335	
gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg	1056
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg	
340 345 350	
aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac	1104
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp	
355 360 365	
caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg	1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro	
370 375 380	
gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa gga	1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	
385 390 395 400	
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgg	1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser	
405 410 415	
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg	1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr	
420 425 430	
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt caa	1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln	
435 440 445	
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca	1386
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
450 455 460	
tag	1389

<210> 6
 <211> 462
 <212> PRT
 <213> *Exophiala spinifera*

<400> 6	
Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu	
1 5 10 15	
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	

<221> CDS

<222> (700)...(1439)

<400> 7

gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg	48
Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu	
1 5 10 15	
gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt	96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
ggc aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcc gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat gtg cga tgc aaa aca g gtgcgtgtgg tgctcgtctca ggtgggggac	676
Gln Tyr Val Arg Cys Lys Thr	

210	215	
tcgtttctca gtgggtcattc cag gt atg cag tcg att tgc cat gcc atg tca		728
	Gly Met Gln Ser Ile Cys His Ala Met Ser	
	220 225	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa		776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu		
	230 235 240	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc		824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala		
	245 250 255	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat		872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr		
	260 265 270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg		920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu		
	275 280 285	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg		968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp		
	290 295 300 305	
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg		1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser		
	310 315 320	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat		1064
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp		
	325 330 335	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag		1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys		
	340 345 350	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa		1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln		
	355 360 365	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc		1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala		
	370 375 380 385	
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct		1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala		
	390 395 400	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg		1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala		
	405 410 415	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag aag tct		1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser		
	420 425 430	

tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt caa cga 1400
 Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg
 435 440 445

ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1442
 Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 8
 <211> 462
 <212> PRT
 <213> *Exophiala spinifera*

<400> 8
 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
 1 5 10 15
 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
 20 25 30
 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 130 135 140
 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 145 150 155 160
 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
 210 215 220
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
 225 230 235 240
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
 245 250 255
 Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu
 260 265 270
 Tyr Pro Thr Leu Thr Phe Ser Pro Leu Pro Ala Glu Lys Gln Ala
 275 280 285
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
 290 295 300
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
 325 330 335
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg

			340					345					350						
Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp				
		355					360					365							
Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro				
	370					375					380								
Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Tyr	Phe	Gln	Gly					
385					390					395				400					
Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser				
				405					410				415						
Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr				
			420					425				430							
Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln				
		435					440					445							
Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala						
	450					455					460								

<210> 9
 <211> 458
 <212> PRT
 <213> Exophiala spinifera

<400> 9

Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu				
1				5					10					15					
Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu				
			20					25				30							
Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly				
		35				40					45								
Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp				
	50					55				60									
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu				
65					70					75				80					
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp				
			85					90				95							
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu				
			100					105				110							
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile				
		115					120					125							
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg				
	130					135					140								
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu				
145					150					155				160					
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly				
			165					170				175							
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys				
		180						185				190							
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly				
		195					200					205							
Gln	Tyr	Val	Arg	Cys	Lys	Thr	Gly	Ala	Cys	Gly	Val	Val	Ser	Gly	Gly				
	210					215					220								
Gly	Leu	Val	Ser	Gln	Trp	Ser	Phe	Gln	Val	Cys	Ser	Arg	Phe	Ala	Met				
225					230					235				240					
Pro	Cys	Gln	Arg	Asn	Leu	Phe	Gln	Ala	Gln	Cys	Thr	Ser	Thr	Pro	Pro				
				245					250					255					
Ser	Leu	Lys	Leu	Ser	Ser	Arg	His	Pro	Ala	Val	Gln	Tyr	Asp	Arg	Pro				
		260						265				270							
Arg	Ala	Pro	Cys	Ser	Glu	Ala	Lys	Arg	Trp	Trp	Phe	Arg	Tyr	Arg	Gln				
		275					280					285							

Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys
 290 295 300
 His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr
 305 310 315 320
 Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn
 325 330 335
 Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser
 340 345 350
 Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly
 355 360 365
 Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr
 370 375 380
 Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg
 385 390 395 400
 Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu
 405 410 415
 Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg
 420 425 430
 Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu
 435 440 445
 Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr
 450 455

<210> 10
 <211> 1392
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> CDS
 <222> (1)...(1389)
 <221> misc_feature
 <222> (1)...(3)
 <223> Extra lysine in K:trAPAO

<400> 10
 aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15
 ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc etc gtt 96
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30
 ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgg 144
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 ggt ccc ggc agg acg act atc aac gac etc ggc gct gcg tgg atc aat 192
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 gag ggc gag etc cag agg acg act gga aat tca atc cat caa gca caa 288

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	

305	310	315	320	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac				1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp				
325		330	335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga				1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly				
340		345	350	
egg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg				1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp				
355		360	365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag				1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu				
370		375	380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa				1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln				
385		390	395	400
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt				1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly				
405		410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag				1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu				
420		425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt				1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly				
435		440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca				1389
Gln Arg Gly Ala Ala Glu Val Ala Ser Leu Val Pro Ala Ala				
450		455	460	

tag 1392

<210> 11
 <211> 463
 <212> PRT
 <213> *Exophiala spinifera*

<400> 11
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95

Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu
			100					105					110		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115					120					125			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
	130					135					140				
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145						150				155					160
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
			165						170					175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180					185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
		195					200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
	210					215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235					240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
			245						250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
		260						265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
		275					280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
	290					295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315					320
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
			325					330						335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
		340						345				350			
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
		355					360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
	370					375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385					390					395					400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
			405						410				415		
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
		420						425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
		435					440					445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
	450					455					460				

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into
expression vectors, N23256

<400> 12

ggggaattca aagacaacgt tgcggacgtg gtag 34

<210> 13
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23259

<400> 13
 ggggcggcgc cctatgctgc tggcaccagg ctag 34

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 3' RACE, N21965

<400> 14
 tggtttcggt accgacaacc ttgtatccc 29

<210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 5' race, N21968

<400> 15
 gagttggtcc cagacagact tttgtcgt 28

<210> 16
 <211> 1673
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> sig_peptide
 <222> (1)...(267)
 <223> yeast alpha mating factor secretion signal.

<221> CDS
 <222> (1)...(1662)

<400> 16
 atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc 48
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 -85 -80 -75

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 96
 Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
 -70 -65 -60

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc	144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe	
-55 -50 -45	
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg	192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu	
-40 -35 -30	
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta	240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val	
-25 -20 -15 -10	
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg	288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala	
-5 1 5	
gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc	336
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg	
10 15 20	
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat	384
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp	
25 30 35	
cgt gta ggg gga aag act ctg agc gta caa tcc ggt ccc ggc agg acg	432
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr	
40 45 50 55	
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc	480
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser	
60 65 70	
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag	528
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln	
75 80 85	
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act	576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr	
90 95 100	
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca	624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala	
105 110 115	
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc	672
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser	
120 125 130 135	
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg	720
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val	
140 145 150	
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc	768
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu	
155 160 165	
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac	816

Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His	
170 175 180	
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt	864
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly	
185 190 195	
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga	912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg	
200 205 210 215	
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt	960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu	
220 225 230	
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag	1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln	
235 240 245	
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga	1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg	
250 255 260	
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg	1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu	
265 270 275	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat	1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn	
280 285 290 295	
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg	1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro	
300 305 310	
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac	1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp	
315 320 325	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg	1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp	
330 335 340	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa	1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln	
345 350 355	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc ccg gca	1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala	
360 365 370 375	
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc	1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu	
380 385 390	
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc	1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala	
395 400 405	

gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgc gcg ctc aga acg	1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr	
410 415 420	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg	1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp	
425 430 435	
aaa ggg tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt gct gca	1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala	
440 445 450 455	
gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c	1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala	
460 465	

<210> 17
 <211> 554
 <212> PRT
 <213> *Exophiala spinifera*

<220>
 <221> SIGNAL
 <222> (1)...(89)

<400> 17	
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser	
-85 -80 -75	
Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln	
-70 -65 -60	
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe	
-55 -50 -45	
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu	
-40 -35 -30	
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val	
-25 -20 -15 -10	
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala	
-5 1 5	
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg	
10 15 20	
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp	
25 30 35	
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr	
40 45 50 55	
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser	
60 65 70	
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln	
75 80 85	
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr	
90 95 100	
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala	
105 110 115	
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser	
120 125 130 135	
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val	
140 145 150	

```

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
      155      160      165
Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
      170      175      180
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
      185      190      195
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
200      205      210      215
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
      220      225      230
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
      235      240      245
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
      250      255      260
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
      265      270      275
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
280      285      290      295
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
      300      305      310
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
      315      320      325
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
      330      335      340
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
      345      350      355
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
360      365      370      375
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
      380      385      390
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
      395      400      405
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
      410      415      420
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
      425      430      435
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
440      445      450      455
Glu Val Val Ala Ser Leu Val Pro Ala Ala
      460      465

```

```

<210> 18
<211> 2079
<212> DNA
<213> Unknown

```

```

<220>
<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
      - 687, gst fusion + polylinker, 688-2076,
      K:trAPAO, extra lysine underlined; 2077-2079, stop
      codon. For bacterial expression.

```

```

<221> CDS
<222> (1)...(2076)

<221> misc_feature
<222> (1)...(687)

```

<223> gst fusion + polylinker

<221> misc_feature

<222> (688)...(2076)

<223> K:trAPAO

<221> misc_feature

<222> (688)...(690)

<223> Extra lysine

<400> 18

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggt gat cat gla acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc	720
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly	
225 230 235 240	
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt	768
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly	
245 250 255	
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act	816
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr	
260 265 270	
ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc	864
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly	
275 280 285	
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt	912
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe	
290 295 300	
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca	960
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser	
305 310 315 320	
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac	1008
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp	
325 330 335	
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc	1056
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro	
340 345 350	
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg	1104
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala	
355 360 365	
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt	1152
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys	
370 375 380	
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc	1200
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile	
385 390 395 400	
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt	1248
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe	
405 410 415	
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg	1296

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser	
420 425 430	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag	1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln	
435 440 445	
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac	1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	
450 455 460	
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca	1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	
465 470 475 480	
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt	1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	
485 490 495	
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt	1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	
500 505 510	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr	
515 520 525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc	1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly	
530 535 540	
ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga	1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg	
545 550 555 560	
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg	1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met	
565 570 575	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga	1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg	
580 585 590	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg	1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly	
595 600 605	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag	1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys	
610 615 620	
cag cag tat ttc caa gga gct ccg aac gcc gtc tat ggg ctg aac gat	1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp	
625 630 635 640	
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat	1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His	
645 650 655	

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg	2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly	
660 665 670	
gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg	2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu	
675 680 685	
gtg cca gca gca tag	2079
Val Pro Ala Ala	
690	

<210> 19
 <211> 692
 <212> PRT
 <213> Unknown

<400> 19

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly	
225 230 235 240	
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly	
245 250 255	
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr	
260 265 270	
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly	
275 280 285	
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe	
290 295 300	

Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	305	310	315	320
Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	325	330	335	
Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	340	345	350	
Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	355	360	365	
Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	370	375	380	
Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	385	390	395	400
Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	405	410	415	
Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	420	425	430	
Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	435	440	445	
Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	450	455	460	
Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	465	470	475	480
Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	485	490	495	
Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	500	505	510	
Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	515	520	525	
Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	530	535	540	
Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	545	550	555	560
Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	565	570	575	
Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	580	585	590	
Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	595	600	605	
Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	610	615	620	
Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	625	630	635	640
Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	645	650	655	
Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	660	665	670	
Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	675	680	685	
Val	Pro	Ala	Ala													690			

<210> 20

<211> 1464

<212> DNA

<213> Unknown

<220>

<223> Nucleotide sequence of K:trAPAO translational

fusion with barley alpha amylase signal sequence,
for expression and secretion of the mature trAPAO
in maize. Nucleotides 1-72, barley alpha amylase
signal sequence, nucleotides 73-75, added lysine
residue; nucleotides 76 -1464 , trAPAO cDNA.

<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

<221> misc_feature
<222> (73)...(1464)
<223> K:trAPAOcDNA

<221> CDS
<222> (1)...(1461)

<221> misc_feature
<222> (73)...(75)
<223> Added lysine residue

```

<400> 20
atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc      48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
          -20                      -15                      -10

ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta      96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
          -5                      1                      5

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag      144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
          10                      15                      20

gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg      192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
          25                      30                      35                      40

gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac      240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
          45                      50                      55

gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc      288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
          60                      65                      70

aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act      336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
          75                      80                      85

gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct      384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
          90                      95                      100

tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa      432
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
          105                      110                      115                      120

```


ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac	480
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp	
125 130 135	
ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg	528
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala	
140 145 150	
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca	576
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala	
155 160 165	
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc	624
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser	
170 175 180	
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat	672
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn	
185 190 195 200	
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca	720
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr	
205 210 215	
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc	768
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly	
220 225 230	
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc	816
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser	
235 240 245	
ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag	864
Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys	
250 255 260	
gtg gtg gtc tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca	912
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser	
265 270 275 280	
cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg	960
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu	
285 290 295	
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc	1008
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg	
300 305 310	
gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca	1056
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser	
315 320 325	
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc	1104
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr	
330 335 340	
tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag	1152

Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys	
345 350 355 360	
cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag	1200
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu	
365 370 375	
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag	1248
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu	
380 385 390	
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg	1296
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly	
395 400 405	
ctg aac gat ctc atc aca ctg ggt tgg gcg ctc aga acg ccg ttc aag	1344
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys	
410 415 420	
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat	1392
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr	
425 430 435 440	
atg gaa ggg gcc ata cga tgg ggt caa cga ggt gct gca gaa gtt gtg	1440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val	
445 450 455	
gct agc ctg gtg cca gca gca tag	1464
Ala Ser Leu Val Pro Ala Ala	
460	

<210> 21
 <211> 487
 <212> PRT
 <213> Unknown

<220>
 <221> SIGNAL
 <222> (1)...(24)

<400> 21	
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly	
-20 -15 -10	
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val	
-5 1 5	
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln	
10 15 20	
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly	
25 30 35 40	
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn	
45 50 55	
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser	
60 65 70	
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr	
75 80 85	
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro	

90		95		100
Tyr Gly Asp Ser Leu	Leu Ser Glu Glu Val	Ala Ser Ala Leu Ala Glu		
105		110		120
Leu Leu Pro Val Trp	Ser Gln Leu Ile Glu Glu	His Ser Leu Gln Asp		
	125		130	135
Leu Lys Ala Ser Pro	Gln Ala Lys Arg Leu Asp	Ser Val Ser Phe Ala		
	140		145	150
His Tyr Cys Glu Lys	Glu Leu Asn Leu Pro Ala Val	Leu Gly Val Ala		
	155		160	165
Asn Gln Ile Thr Arg	Ala Leu Leu Gly Val Glu Ala	His Glu Ile Ser		
	170		175	180
Met Leu Phe Leu Thr	Asp Tyr Ile Lys Ser Ala Thr	Gly Leu Ser Asn		
185		190		200
Ile Phe Ser Asp Lys	Lys Asp Gly Gly Gln Tyr Met Arg	Cys Lys Thr		
	205		210	215
Gly Met Gln Ser Ile	Cys His Ala Met Ser Lys Glu Leu Val	Pro Gly		
	220		225	230
Ser Val His Leu Asn	Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser			
	235		240	245
Gly Cys Thr Val Arg	Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys			
	250		255	260
Val Val Val Ser Leu	Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser			
265		270		275
Pro Pro Leu Pro Ala	Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu			
	285		290	295
Gly Tyr Tyr Ser Lys	Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg			
	300		305	310
Glu Gln Gly Phe Ser	Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser			
	315		320	325
Phe Ala Arg Asp Thr	Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr			
	330		335	340
Cys Phe Met Val Gly	Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys			
345		350		355
Gln Val Arg Gln Lys	Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu			
	365		370	375
Asn Ala Gly Ala Gln	Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu			
	380		385	390
Trp Ser Lys Gln Gln	Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly			
	395		400	405
Leu Asn Asp Leu Ile	Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys			
	410		415	420
Ser Val His Phe Val	Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr			
425		430		435
Met Glu Gly Ala Ile	Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val			
	445		450	455
Ala Ser Leu Val Pro	Ala Ala			
	460			

<210> 22
 <211> 1803
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> CDS
 <222> (1)...(1800)

<400> 22

atg gca ctt gca ccg agc tac atc aat ccc cca aac gtc gcc tcc cca	48
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro	
1 5 10 15	
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg	96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
aca ata gct gga cag att gga caa gac gct tgc ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg	336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	
cca gtg tgc gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
115 120 125	
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg	432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
130 135 140	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
145 150 155 160	
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165 170 175	
ggg gga aag act ctg agc gta caa tgc ggt ccc ggc agg acg act atc	576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
180 185 190	
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta	624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val	
195 200 205	
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg	672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	
210 215 220	
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct	720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala	

225	230	235	240	
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245 250 255				768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260 265 270				816
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275 280 285				864
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290 295 300				912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305 310 315 320				960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325 330 335				1008
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340 345 350				1056
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355 360 365				1104
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370 375 380				1152
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385 390 395 400				1200
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405 410 415				1248
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 420 425 430				1296
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 435 440 445				1344
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450 455 460				1392

tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att	1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
465 470 475 480	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
485 490 495	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac	1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
500 505 510	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
515 520 525	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
530 535 540	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc	1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
545 550 555 560	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg	1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
565 570 575	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt	1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
580 585 590	
gtg gct agc ctg gtg cca gca gca tag	1803
Val Ala Ser Leu Val Pro Ala Ala	
595 600	

<210> 23

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 23

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro	
1 5 10 15	
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	

Val Ala Ser Leu Val Pro Ala Ala
580 585 590
595 600

<210> 24
<211> 3003
<212> DNA
<213> Unknown

<220>
<223> Sequence is barley alpha amylase signal sequence:
espl mat: an artificial spacer sequence and
K:trAPAO

<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

<221> misc_feature
<222> (73)...(1575)
<223> espl mat

<221> misc_feature
<222> (1576)...(1611)
<223> spacer sequence

<221> misc_feature
<222> (1612)...(3000)
<223> K:trAPAO

<221> CDS
<222> (1)...(3000)

<221> misc_feature
<222> (1612)...(1614)
<223> Extra lysine

<400> 24
atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc 48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
-20 -15 -10
ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct 96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
-5 1 5
ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc 144
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
10 15 20
gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt 192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
25 30 35 40
gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act 240
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
45 50 55

gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc	288
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu	
60 65 70	
cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt	336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly	
75 80 85	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag	384
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	
90 95 100	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa	432
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu	
105 110 115 120	
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc	480
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala	
125 130 135	
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg	528
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu	
140 145 150	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg	576
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly	
155 160 165	
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca	624
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	
170 175 180	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg	672
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala	
185 190 195 200	
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca	720
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro	
205 210 215	
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc	768
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe	
220 225 230	
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc	816
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu	
235 240 245	
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat	864
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp	
250 255 260	
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag	912
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu	
265 270 275 280	
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc	960

Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg	
285 290 295	
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc	1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala	
300 305 310	
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat	1056
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr	
315 320 325	
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt	1104
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu	
330 335 340	
gga gca tat ccc att gga tcc cca ggg atc gga tcc cct caa gat cag	1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln	
345 350 355 360	
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc	1200
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile	
365 370 375	
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac	1248
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr	
380 385 390	
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg	1296
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val	
395 400 405	
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca	1344
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala	
410 415 420	
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc	1392
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala	
425 430 435 440	
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa	1440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln	
445 450 455	
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt	1488
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val	
460 465 470	
gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt	1536
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg	
475 480 485	
tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc	1584
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly	
490 495 500	
agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg	1632
Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val	
505 510 515 520	

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 525 530 535	1680
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 540 545 550	1728
ggg gga aag act ctg agc gta caa tgc ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 555 560 565	1776
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 570 575 580	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 585 590 595 600	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 605 610 615	1920
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tgc gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tgc att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730 735 740	2304
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tgc gca	2352

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	
745 750 755 760	
tcc ggc tgt aca gta cga tgc gcc tgc ggc gcc gtg ttc cga agc aaa	2400
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	
765 770 775	
aag gtg gtg gtt tgc tta ccg aca acc ttg tat ccc acc ttg aca ttt	2448
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
780 785 790	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc	2496
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
795 800 805	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg	2544
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
810 815 820	
cgc gaa caa ggc ttc tgc ggc gtc ctc caa tgc agc tgt gac ccc atc	2592
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
825 830 835 840	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att	2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
845 850 855	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
860 865 870	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac	2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
875 880 885	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
890 895 900	
gag tgg tgc aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
905 910 915 920	
ggg ctg aac gat ctc atc aca ctg ggt tgc gcg ctc aga acg ccg ttc	2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
925 930 935	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg	2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
940 945 950	
tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt	2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
955 960 965	
gtg gct agc ctg gtg cca gca gca tag	3003
Val Ala Ser Leu Val Pro Ala Ala	

<210> 25
 <211> 1000
 <212> PRT
 <213> Unknown

<220>
 <221> SIGNAL
 <222> (1)...(24)

<400> 25

Met	Ala	Asn	Lys	His	Leu	Ser	Leu	Ser	Leu	Phe	Leu	Val	Leu	Leu	Gly
				-20					-15					-10	
Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Ala	Pro	Thr	Val	Lys	Ile	Asp	Ala
			-5					1				5			
Gly	Met	Val	Val	Gly	Thr	Thr	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr
	10				15						20				
Val	Ser	Glu	Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala	Ser	Pro	Thr	Arg	Phe
25				30					35					40	
Ala	Pro	Pro	Thr	Arg	Pro	Val	Pro	Trp	Ser	Thr	Pro	Leu	Gln	Ala	Thr
			45					50					55		
Ala	Tyr	Gly	Pro	Ala	Cys	Pro	Gln	Gln	Phe	Asn	Tyr	Pro	Glu	Glu	Leu
			60					65					70		
Arg	Glu	Ile	Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro	Pro	Pro	Ser	Ala	Gly
	75						80					85			
Glu	Ser	Glu	Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu
	90					95					100				
Asn	Thr	Asn	Lys	Ala	Val	Met	Val	Trp	Ile	Tyr	Gly	Gly	Ala	Leu	Glu
105				110						115				120	
Tyr	Gly	Trp	Asn	Ser	Phe	His	Leu	Tyr	Asp	Gly	Ala	Ser	Phe	Ala	Ala
			125						130					135	
Asn	Gln	Asp	Val	Ile	Ala	Val	Thr	Ile	Asn	Tyr	Arg	Thr	Asn	Ile	Leu
			140					145					150		
Gly	Phe	Pro	Ala	Ala	Pro	Gln	Leu	Pro	Ile	Thr	Gln	Arg	Asn	Leu	Gly
		155					160					165			
Phe	Leu	Asp	Gln	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile	Ala
	170					175					180				
Ala	Phe	Gly	Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala
185					190					195				200	
Gly	Gly	Arg	Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro
			205						210					215	
Pro	Phe	Arg	Ala	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn	Phe
			220					225					230		
Pro	Lys	Gly	Asp	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala	Leu
	235						240					245			
Asn	Cys	Thr	Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp
250						255					260				
Leu	Ala	Thr	Leu	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Gly	Phe	Glu
265					270					275				280	
Tyr	Thr	Leu	Asp	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala	Arg
			285						290					295	
Thr	Thr	Gly	Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala
			300					305					310		
Asn	Asp	Gly	Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr
	315						320					325			
Leu	Glu	Glu	Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu

330		335		340
Gly Ala Tyr Pro Ile	Gly Ser Pro Gly Ile	Gly Ser Pro Gln Asp Gln		
345	350	355	360	
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe	Gln Cys Pro Ser Ala Ile			
365	370	375		
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile	Pro Ser Trp Arg Tyr Tyr			
380	385	390		
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe	Pro Gly Ser Glu Val			
395	400	405		
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr	Tyr Pro Val Ala			
410	415	420		
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met	Gln Gly Ala			
425	430	435	440	
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly	Pro Gly Trp Lys Gln			
445	450	455		
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala	Ile Gln Val			
460	465	470		
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg				
475	480	485		
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly				
490	495	500		
Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val				
505	510	515	520	
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val				
525	530	535		
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val				
540	545	550		
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile				
555	560	565		
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val				
570	575	580		
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr				
585	590	595	600	
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala				
605	610	615		
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Val Ala Ser Ala Leu Ala				
620	625	630		
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln				
635	640	645		
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe				
650	655	660		
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val				
665	670	675	680	
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile				
685	690	695		
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser				
700	705	710		
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys				
715	720	725		
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro				
730	735	740		
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala				
745	750	755	760	
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys				
765	770	775		
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe				
780	785	790		
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile				

<400> 26

atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc	48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly	
-20 -15 -10	
ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc	96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr	
-5 1 5	
gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc	144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg	
10 15 20	
gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg	192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro	
25 30 35 40	
ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt	240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe	
45 50 55	
ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc	288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala	
60 65 70	
ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca	336
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser	
75 80 85	
ggc gct aaa ccc gcc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc	384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	
90 95 100	
ggc ttc gcc gcc gcc acg gcc gcc atg ccc tac tac gac ggc gag gcg	432
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	
105 110 115 120	
ctt gcg cga cag gcc gtc gtc gtg gtg acg ttt aac tat cgg acg aac	480
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn	
125 130 135	
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc	528
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr	
140 145 150	
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg	576
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg	
155 160 165	
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc gcc cga gtg	624
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val	
170 175 180	
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc	672
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu	
185 190 195 200	

acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt	720
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser	
205 210 215	
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg	768
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser	
220 225 230	
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca	816
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro	
235 240 245	
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac	864
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp	
250 255 260	
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg	912
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu	
265 270 275 280	
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt	960
Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val	
285 290 295	
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg	1008
Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly	
300 305 310	
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg	1056
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala	
315 320 325	
cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac	1104
Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp	
330 335 340	
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc gcc gac aat	1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn	
345 350 355 360	
cag ttc aat ccg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag	1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln	
365 370 375	
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga	1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly	
380 385 390	
aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg	1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val	
395 400 405	
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc	1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro	
410 415 420	
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc	1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val	

425	430	435	440	
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct				1410
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro				
	445	450	455	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc				1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg				
	460	465	470	
gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc				1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly				
	475	480	485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc				1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser				
	490	495	500	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt				1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly				
	505	510	515	520
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt				1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val				
	525	530	535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg				1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser				
	540	545	550	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat				1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn				
	555	560	565	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg				1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu				
	570	575	580	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa				1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln				
	585	590	595	600
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag				1920
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu				
	605	610	615	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg				1968
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu				
	620	625	630	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag				2016
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys				
	635	640	645	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac				2064
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn				
	650	655	660	

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 665 670 675 680	2112
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 685 690 695	2160
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 700 705 710	2208
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 715 720 725	2256
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 730 735 740	2304
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 745 750 755 760	2352
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 765 770 775	2400
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 780 785 790	2448
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 795 800 805	2496
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gcc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 810 815 820	2544
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 825 830 835 840	2592
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 845 850 855	2640
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 860 865 870	2688
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 875 880 885	2736
cgg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 890 895 900	2784

890	895	900	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			2832
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
905	910	915	920
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag			2880
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
	925	930	935
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			2928
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
	940	945	950
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca			2973
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
	955	960	965
tag			2976
<210> 27			
<211> 991			
<212> PRT			
<213> Unknown			
<220>			
<221> SIGNAL			
<222> (1)...(24)			
<400> 27			
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly			
	-20	-15	-10
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr			
	-5	1	5
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg			
10	15	20	
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro			
25	30	35	40
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe			
	45	50	55
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala			
	60	65	70
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser			
	75	80	85
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly			
90	95	100	
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala			
105	110	115	120
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn			
	125	130	135
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr			
	140	145	150
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg			
	155	160	165
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val			
170	175	180	
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu			
185	190	195	200

Thr	Ser	Pro	Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser	205	210	215
Pro	Gly	Leu	Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser	220	225	230
Gly	Glu	Arg	Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro	235	240	245
Ala	Thr	Leu	Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp	250	255	260
Leu	Arg	Arg	Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	265	270	275
Pro	Gln	Thr	Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	285	290	295
Arg	Val	Leu	Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	300	305	310
Arg	Ala	Pro	Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala	315	320	325
Gln	Phe	Gly	Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp	330	335	340
Gly	Arg	Ala	Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	345	350	355
Gln	Phe	Asn	Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	365	370	375
Gly	Ala	Pro	Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	380	385	390
Arg	Ala	Pro	Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	395	400	405
Phe	Lys	Leu	Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	410	415	420
Thr	Pro	Ala	Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	425	430	435
Arg	Phe	Ala	Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	445	450	455
Ala	Tyr	Ser	Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg	460	465	470
Ala	Ala	Val	Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly	475	480	485
Ala	Lys	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	490	495	500
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	505	510	515
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	525	530	535
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	540	545	550
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	555	560	565
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	570	575	580
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	585	590	595
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	605	610	615
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	620	625	630
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	635	640	645
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	650	655	660

```

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
665                      670                      675                      680
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
                      685                      690                      695
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
                      700                      705                      710
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
                      715                      720                      725
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
                      730                      735                      740
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745                      750                      755                      760
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
                      765                      770                      775
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
                      780                      785                      790
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
                      795                      800                      805
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
810                      815                      820
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825                      830                      835                      840
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                      845                      850                      855
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
                      860                      865                      870
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
                      875                      880                      885
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
890                      895                      900
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905                      910                      915                      920
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
                      925                      930                      935
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
                      940                      945                      950
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
955                      960                      965

```

```

<210> 28
<211> 3618
<212> DNA
<213> Unknown

```

```

<220>
<223> gst:esp1:sp:K:trapao, 3618. 1-687, gst +
polylinker; 688-2190, esp1 mat; 2191-2226 spacer;
2227-3615, K:trAPAO, 3616-3618, stop codon. For
bacterial expression.

```

```

<221> CDS
<222> (1)...(3615)
<221> misc_feature
<222> (1)...(687)
<223> gst + polylinker

```

<221> mat_peptide
 <222> (688)...(2190)
 <223> espl mat

<221> misc_feature
 <222> (2191)...(2226)
 <223> spacer sequence

<221> misc_feature
 <222> (2227)...(3615)
 <223> K:trAPAO

<221> misc_feature
 <222> (2227)...(2229)
 <223> Extra lysine

<400> 28
 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt 336
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 aaa gar ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta 528

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc gct cct act gtc aag att gat gct ggg atg gtg	720
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val	
225 230 235 240	
gtc ggc acg act act act gtc ccc ggc acc act gcg acc gtc agc gag	768
Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu	
245 250 255	
ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt gcg cct cct	816
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro	
260 265 270	
act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act gca tat ggt	864
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly	
275 280 285	
cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc cgt gag att	912
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile	
290 295 300	
acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt gaa agt gag	960
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu	
305 310 315 320	
gac tgc ctg aac ctc aac atc tac gtc cca gga act gag aac aca aac	1008
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn	
325 330 335	
aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa tat ggt tgg	1056
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp	
340 345 350	
aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc aat cag gat	1104
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp	
355 360 365	
gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct	1152
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro	
370 375 380	
gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac	1200
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp	
385 390 395 400	

caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca gcc ttt ggc Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly 405 410 415	1248
ggc gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg 420 425 430	1296
agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca ccc ttc cga Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg 435 440 445	1344
gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc ccc aag gga Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly 450 455 460	1392
gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr 465 470 475 480	1440
acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr 485 490 495	1488
ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu 500 505 510	1536
gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc acg act ggt Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly 515 520 525	1584
gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc aac gac gga Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly 530 535 540	1632
ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat ctc gag gag Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu 545 550 555 560	1680
gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr 565 570 575	1728
ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala 580 585 590	1776
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln 595 600 605	1824
gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala 610 615 620	1872
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc	1920

Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser	
625 630 635 640	
tet gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc	1968
Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr	
645 650 655	
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc	2016
Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala	
660 665 670	
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat	2064
Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn	
675 680 685	
gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct	2112
Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser	
690 695 700	
cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act	2160
Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr	
705 710 715 720	
gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc agc ggc gga	2208
Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly	
725 730 735	
ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg	2256
Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val	
740 745 750	
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc	2304
Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala	
755 760 765	
ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag	2352
Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys	
770 775 780	
act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc	2400
Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu	
785 790 795 800	
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg	2448
Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu	
805 810 815	
ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat	2496
Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn	
820 825 830	
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt	2544
Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly	
835 840 845	
gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc	2592
Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu	
850 855 860	

ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag	2640
Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys	
865 870 875 880	
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac	2688
Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr	
885 890 895	
tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag	2736
Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln	
900 905 910	
atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt	2784
Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu	
915 920 925	
ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc	2832
Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe	
930 935 940	
tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg	2880
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met	
945 950 955 960	
cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg	2928
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val	
965 970 975	
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt	2976
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys	
980 985 990	
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg	3024
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val	
995 1000 1005	
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct	3072
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro	
1010 1015 1020	
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac	3120
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr	
1025 1030 1035 1040	
tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa	3168
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln	
1045 1050 1055	
ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc	3216
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala	
1060 1065 1070	
aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc	3264
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe	
1075 1080 1085	
atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta	3312

Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val	
1090	1095 1100
cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc	3360
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala	
1105	1110 1115 1120
ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg	3408
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser	
	1125 1130 1135
aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac	3456
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn	
	1140 1145 1150
gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt	3504
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val	
	1155 1160 1165
cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa	3552
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu	
	1170 1175 1180
ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc	3600
Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser	
1185	1190 1195 1200
ctg gtg cca gca gca tag	3618
Leu Val Pro Ala Ala	
	1205

<210> 29
 <211> 1205
 <212> PRT
 <213> Unknown

<400> 29	
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1	5 10 15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
	20 25 30
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
	35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
	50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65	70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
	85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
	100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
	115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
	130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145	150 155 160

Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
				165					170					175	
Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
			180					185						190	
Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
		195					200					205			
Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210					215					220				
Gly	Ser	Pro	Glu	Phe	Ala	Pro	Thr	Val	Lys	Ile	Asp	Ala	Gly	Met	Val
225					230					235					240
Val	Gly	Thr	Thr	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr	Val	Ser	Glu
				245					250					255	
Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala	Ser	Pro	Thr	Arg	Phe	Ala	Pro	Pro
			260					265					270		
Thr	Arg	Pro	Val	Pro	Trp	Ser	Thr	Pro	Leu	Gln	Ala	Thr	Ala	Tyr	Gly
		275					280					285			
Pro	Ala	Cys	Pro	Gln	Gln	Phe	Asn	Tyr	Pro	Glu	Glu	Leu	Arg	Glu	Ile
	290					295					300				
Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro	Pro	Pro	Ser	Ala	Gly	Glu	Ser	Glu
305					310					315					320
Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu	Asn	Thr	Asn
			325						330					335	
Lys	Ala	Val	Met	Val	Trp	Ile	Tyr	Gly	Gly	Ala	Leu	Glu	Tyr	Gly	Trp
			340					345						350	
Asn	Ser	Phe	His	Leu	Tyr	Asp	Gly	Ala	Ser	Phe	Ala	Ala	Asn	Gln	Asp
		355					360					365			
Val	Ile	Ala	Val	Thr	Ile	Asn	Tyr	Arg	Thr	Asn	Ile	Leu	Gly	Phe	Pro
	370					375					380				
Ala	Ala	Pro	Gln	Leu	Pro	Ile	Thr	Gln	Arg	Asn	Leu	Gly	Phe	Leu	Asp
385					390					395					400
Gln	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile	Ala	Ala	Phe	Gly
			405						410					415	
Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala	Gly	Gly	Arg
			420					425					430		
Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro	Pro	Phe	Arg
		435					440					445			
Ala	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn	Phe	Pro	Lys	Gly
	450					455					460				
Asp	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala	Leu	Asn	Cys	Thr
465					470					475					480
Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp	Leu	Ala	Thr
			485						490					495	
Leu	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Gly	Phe	Glu	Tyr	Thr	Leu
			500					505					510		
Asp	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala	Arg	Thr	Thr	Gly
		515					520					525			
Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala	Asn	Asp	Gly
	530					535					540				
Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr	Leu	Glu	Glu
545					550					555					560
Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu	Gly	Ala	Tyr
			565						570					575	
Pro	Ile	Gly	Ser	Pro	Gly	Ile	Gly	Ser	Pro	Gln	Asp	Gln	Ile	Ala	Ala
			580					585					590		
Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala	Ile	Val	Ala	Gln
		595					600					605			
Asp	Ser	Arg	Asn	Arg	Gly	Ile	Pro	Ser	Trp	Arg	Tyr	Tyr	Tyr	Asn	Ala
	610					615						620			

Thr	Phe	Glu	Asn	Leu	Glu	Leu	Phe	Pro	Gly	Ser	Glu	Val	Tyr	His	Ser	625	630	635	640
Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val	Ala	Ser	Ala	Thr	645	650	655	
Ala	Leu	Glu	Ala	Gln	Thr	Ser	Lys	Tyr	Met	Gln	Gly	Ala	Trp	Ala	Ala	660	665	670	
Phe	Ala	Lys	Asn	Pro	Met	Asn	Gly	Pro	Gly	Trp	Lys	Gln	Val	Pro	Asn	675	680	685	
Val	Ala	Ala	Leu	Gly	Ser	Pro	Gly	Lys	Ala	Ile	Gln	Val	Asp	Val	Ser	690	695	700	
Pro	Ala	Thr	Ile	Asp	Gln	Arg	Cys	Ala	Leu	Tyr	Thr	Arg	Tyr	Tyr	Thr	705	710	715	720
Glu	Leu	Gly	Thr	Ile	Ala	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Ser	Gly	Gly	725	730	735	
Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	740	745	750	
Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	755	760	765	
Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	770	775	780	
Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	785	790	795	800
Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	805	810	815	
Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	820	825	830	
Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	835	840	845	
Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	850	855	860	
Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	865	870	875	880
Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	885	890	895	
Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	900	905	910	
Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	915	920	925	
Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	930	935	940	
Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	945	950	955	960
Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	965	970	975	
His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	980	985	990	
Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	995	1000	1005	
Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	1010	1015	1020	
Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	1025	1030	1035	1040
Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	1045	1050	1055	
Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	1060	1065	1070	
Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	1075	1080	1085	

Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val
 1090 1095 1100
 Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala
 1105 1110 1115 1120
 Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser
 1125 1130 1135
 Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn
 1140 1145 1150
 Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val
 1155 1160 1165
 His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu
 1170 1175 1180
 Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser
 1185 1190 1195 1200
 Leu Val Pro Ala Ala
 1205

<210> 30
 <211> 3591
 <212> DNA
 <213> Unknown

<220>
 <223> Open reading frame of BEST1:K:trAPAO fusion for
 bacterial expression vector pGEX-4T-1 or similar
 vector. gst:BST1:sp:K:trAPAO fusion, 3591 nt.
 1-687 gst
 + polylinker, 688-2163, BEST1 mature; 2164-2199,
 spacer, 2200-3588, K:trAPAO

<221> misc_feature
 <222> (1)...(687)
 <223> gst + polylinker

<221> mat_peptide
 <222> (688)...(2163)
 <223> BEST1 mature

<221> misc_feature
 <222> (2164)...(2199)
 <223> spacer sequence

<221> misc_feature
 <222> (2200)...(3588)
 <223> K:trAPAO

<221> CDS
 <222> (1)...(3588)

<221> misc_feature
 <222> (2200)...(2202)
 <223> Extra lysine

<400> 30
 atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

48

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tgc aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt gcc gac cat cct cca aaa tgc gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc acg gat ttt ccg gtc ccg agg acc gat ctg gcc	720
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly	
225 230 235 240	
cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt ccg gga ata ccc	768

Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro	
245 250 255	
tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg ccc caa cac	816
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His	
260 265 270	
gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt ggc tcc gac	864
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp	
275 280 285	
tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc ccc ggc gtg	912
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val	
290 295 300	
agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca ggc gct aaa	960
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys	
305 310 315 320	
ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc ggc ttc gcc	1008
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala	
325 330 335	
ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg ctt gcg cga	1056
Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg	
340 345 350	
cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac atc ctg ggc	1104
Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly	
355 360 365	
ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc gga act tcg	1152
Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser	
370 375 380	
ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg tgg gtg cag	1200
Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln	
385 390 395 400	
agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt	1248
Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe	
405 410 415	
ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg	1296
Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro	
420 425 430	
ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg	1344
Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu	
435 440 445	
acg cga ccg ctc gcg arg ctc gcc gac agc gcc gcc tcg ggc gag cgc	1392
Thr Arg Pro Leu Ala Thr Ala Asp Ser Ala Ala Ser Gly Glu Arg	
450 455 460	
ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg	1440
Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu	
465 470 475 480	

atg gcg cgc gcc gac gcg gcc cgc ccg gca tgc egg gac ctg cgc agg	1488
Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg	
485 490 495	
ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg ccg cag acc	1536
Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr	
500 505 510	
gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt cgg gtc ctg	1584
Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu	
515 520 525	
atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg cgc gcg ccg	1632
Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro	
530 535 540	
atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg cag ttt ggc	1680
Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly	
545 550 555 560	
gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac ggc cgg gcc	1728
Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala	
565 570 575	
acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat cag ttc aat	1776
Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn	
580 585 590	
egg ggg gtc tgc gcc ttc tgc gaa gcg ctt gtg cgc cag ggc gcg ccc	1824
Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro	
595 600 605	
gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga aga gcg ccg	1872
Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro	
610 615 620	
gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg ttc aag ctc	1920
Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu	
625 630 635 640	
gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc acg ccc gcc	1968
Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala	
645 650 655	
gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc cgg ttc gcc	2016
Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala	
660 665 670	
aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct gcc tat tct	2064
Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser	
675 680 685	
acg ggc aag tgc acc atg aca ttc ggt ccc gag ggc cgc gcg gcg gtg	2112
Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val	
690 695 700	
gtg tgc ccc gga cct tcc atc ccc cct tgc gcg gat ggc gcc aag gcg	2160

Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala	
705 710 715 720	
ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac aac	2208
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn	
725 730 735	
gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg	2256
Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr	
740 745 750	
gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag ggc	2304
Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala	
755 760 765	
atg gat cgt gta ggg gga aag act ctg agc gta caa tgc ggt ccc ggc	2352
Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly	
770 775 780	
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac	2400
Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn	
785 790 795 800	
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag	2448
Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu	
805 810 815	
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca	2496
Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr	
820 825 830	
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca	2544
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala	
835 840 845	
agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag	2592
Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu	
850 855 860	
cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac	2640
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp	
865 870 875 880	
agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct	2688
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala	
885 890 895	
gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa	2736
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu	
900 905 910	
gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc	2784
Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala	
915 920 925	
acc ggt ctc agt aat att ttc tgc gac aag aaa gac ggc ggg cag tat	2832
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr	
930 935 940	

atg cga tgc aaa aca ggt atg cag tgc att tgc cat gcc atg tca aag	2880
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys	
945 950 955 960	
 gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att	2928
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile	
965 970 975	
 gag cag tgc gca tcc ggc tgt aca gta cga tgc gcc tgc ggc gcc gtg	2976
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val	
980 985 990	
 ttc cga agc aaa aag gtg gtg gtt tgc tta ccg aca acc ttg tat ccc	3024
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro	
995 1000 1005	
 acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg	3072
Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala	
1010 1015 1020	
 gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac	3120
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp	
1025 1030 1035 1040	
 aag ccg tgg tgg cgc gaa caa ggc ttc tgc ggc gtc ctc caa tgc agc	3168
Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser	
1045 1050 1055	
 tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga	3216
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg	
1060 1065 1070	
 caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg	3264
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp	
1075 1080 1085	
 tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc	3312
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu	
1090 1095 1100	
 cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac	3360
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn	
1105 1110 1115 1120	
 gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa gga gct ccg	3408
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro	
1125 1130 1135	
 agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgc gcg ctc	3456
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu	
1140 1145 1150	
 aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta	3504
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu	
1155 1160 1165	
 gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt	3552

Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly
 1170 1175 1180

gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag
 Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 1185 1190 1195

3591

<210> 31
 <211> 1196
 <212> PRT
 <213> Unknown

<400> 31
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly
 225 230 235 240
 Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro
 245 250 255
 Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His
 260 265 270
 Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp
 275 280 285
 Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val
 290 295 300
 Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys
 305 310 315 320
 Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala
 325 330 335
 Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg
 340 345 350

Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr
 820 825 830
 Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala
 835 840 845
 Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu
 850 855 860
 His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp
 865 870 875 880
 Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala
 885 890 895
 Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu
 900 905 910
 Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala
 915 920 925
 Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr
 930 935 940
 Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys
 945 950 955 960
 Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile
 965 970 975
 Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val
 980 985 990
 Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro
 995 1000 1005
 Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala
 1010 1015 1020
 Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp
 1025 1030 1035 1040
 Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser
 1045 1050 1055
 Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg
 1060 1065 1070
 Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp
 1075 1080 1085
 Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu
 1090 1095 1100
 Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn
 1105 1110 1115 1120
 Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro
 1125 1130 1135
 Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu
 1140 1145 1150
 Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu
 1155 1160 1165
 Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly
 1170 1175 1180
 Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 1185 1190 1195

<210> 32
 <211> 1803
 <212> DNA
 <213> Unknown

 <220>
 <221> CDS
 <222> (1)...(1803)

<223> Glyc(-)APAO coding sequence; mutation in putative
glycosylation sites

```

<400> 32
atg gca ctt gca ccg agc tac atc aat ccc cca aac gtc gcc tcc cca      48
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
  1             5             10             15

gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg      96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
             20             25             30

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct      144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
             35             40             45

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc      192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
             50             55             60

ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac      240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
             65             70             75             80

tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg      288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
             85             90             95

ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg      336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
             100            105            110

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc      384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
             115            120            125

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg      432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
             130            135            140

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc      480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
             145            150            155            160

cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta      528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
             165            170            175

ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc      576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
             180            185            190

aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta      624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val
             195            200            205

tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg      672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr

```


210	215	220	
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct			720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala			
225	230	235	240
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg			768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala			
	245	250	255
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa			816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln			
	260	265	270
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc			864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe			
	275	280	285
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta			912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val			
	290	295	300
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc			960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile			
	305	310	315
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt			1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser			
	325	330	335
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa			1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys			
	340	345	350
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca			1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro			
	355	360	365
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca			1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			
	370	375	380
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa			1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
	385	390	395
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt			1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
	405	410	415
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc			1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
	420	425	430
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg			1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
	435	440	445

cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450 455 460	1392
tea ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 465 470 475 480	1440
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 485 490 495	1488
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 500 505 510	1536
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 515 520 525	1584
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 530 535 540	1632
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 545 550 555 560	1680
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 565 570 575	1728
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 580 585 590	1776
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala *	1803
595 600	

<210> 33
 <211> 600
 <212> PRT
 <213> Unknown

<400> 33
 Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1 5 10 15
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly

545 550 555 560
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 34
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> 37-mer oligonucleotide

<400> 34
 gggaattca tggcacttgc accgagctac atcaatc

37

<210> 35
 <211> 1929
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
 <222> (1134)...(1186)

<400> 35
 atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc aggggtattcc 60
 cacatcggcg taggccc aaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa 120
 gacgctttgg gcgtgacaga ccagcctac gagaaacagg ttgcccaagc attgccaat 180
 ctgcgagcct gccttgctgc agttggagcc tcttcaaaag acgtcaccaa gctcaattac 240
 tacatcgtcg actacgcccc gagcaaaactc accgcaattg gagatgggct gaagtctacc 300
 tttgcccttg acaggctccc tctttgcacg ctgggtgccag taccggcctt ggettcacct 360
 gaatacctct ttgaggttga tgccacggcg ctgggtgccag gacactcgac ccagacaaac 420
 gttgcggacg tggtagtggt gggcgctggc ttgagcgggt tggagacggc acgcaaagtc 480
 caggccgccc gtctgtctcg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact 540
 ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600
 aatgacagca accaaaagcga agtatccaga ttgtttgaaa gatttcattt ggagggcgag 660
 ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720
 ccttatggtg actccccggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt 780
 agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840
 ggaactcctc cccgtatggt ctcaactgat cgaagagtat agccttgaag accccaaggc 900
 gagccctcag gcgaagcggc tcgacagtgt gagcttcgag cactactgtg agaaggacct 960
 aaacttgcct gctgttctca gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020
 agcccaagag atcagcatgc tttttctcac cgactacatc aagagtgcga ccggtctcag 1080
 taatattgtc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgctg 1140
 cgggtgtctc tcaggtaggy gactcgtttc ttagtggtca ttccaggtat gcagtgcatt 1200
 tgccatgcca tgtcaaagga acttgtttcc ggctcagtg cactcaaac cccgctgcct 1260
 ggaattgagc agtcggcggt cggctgtata gtaagatgg cctcgggcgc cgtgttccga 1320
 agcaaaaagg tgggtggttc gttaccgaca acattgtatc ccacttgac attttccaca 1380
 cctcttcccc ccgagaagca agcattggcg gaaaaatcta tctcgggcta ctatagcaag 1440
 atagtcttcg tatgggacaa cccgtgggtg cgcgaacaag gcttctcggg cgtcctccaa 1500
 tcgagctgtg acccatctc atttgccaga gataaccaga tcgaagtcca tcggcaatgg 1560

tccattacct gtttcatggt cggagacccg ggacggaagt ggtcccaaca gtccaagcag	1620
gtacgacaaa agtctgtctg ggaccaactc cgcgcagcct acgagaacgc cggggcccaa	1680
gtcccagagc cggccaacgt gtcgaaatc gagtggtcga agcagcagta tttccaagga	1740
gctccgagcg ccgtctatgg gctgaacgat ctcatcacac tgggttcggc gctcagaacg	1800
ccgttcaagt gtgttcattt cgttggaacg gagacgtctt tagtttggaa agggatatg	1860
gaaggggcca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctggtgcc	1920
gcagcatag	1929

<210> 36

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 36

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro	1	5	10	15
Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val	20	25	30	
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro	35	40	45	
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys	50	55	60	
Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr	65	70	75	80
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	85	90	95	
Leu	Lys	Ser	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	100	105	110	
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala	115	120	125	
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	130	135	140	
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	145	150	155	160
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	165	170	175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	180	185	190	
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	195	200	205	
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	210	215	220	
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	225	230	235	240
Pro	Tyr	Gly	Asp	Ser	Pro	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	245	250	255	
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	Tyr	Ser	Leu	Glu	260	265	270	
Asp	Pro	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	275	280	285	
Ala	His	Tyr	Cys	Glu	Lys	Asp	Leu	Asn	Leu	Pro	Ala	Val	Leu	Ser	Val	290	295	300	
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	305	310	315	320
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	325	330	335	
Asn	Ile	Val	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	340	345	350	

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
 370 375 380
 Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
 420 425 430
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
 435 440 445
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460
 Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
 465 470 475 480
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560
 Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 37
 <211> 1929
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
 <222> (1134)...(1186)

<400> 37
 atggcacttg caccgageta catcaatccc ccaaactgctg cctccccagc aggggtattcc
 cacatcgggc taggccc aaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa
 gacgctttgg gcgtgacaga cccagcctac gagaaacagg ttgcccagc attcgccaat
 ctgagagctt gccttgctgc agttggagcc tcttcaaagc acgtcaccaa gctcaattac
 tacatcgtcg actacgcccc gagcaaaactc accgcaattg gagatgggct gaagtctacc
 tttgcccctt acaggctccc tcttgacag ctggtgccag taccggcctt ggcttcacct
 gaatacctct ttgaggttga cgccacggcg ctgggtgccag gacactcgac cccagacaa
 gttgcggacg tggtagtggt gggcgctggc ttgagcggt tggagacggc acgcaaagtc
 caggccgccc gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaaagact
 ctgagcgtac aatcgggtec cggcaggacg actatcaacg acctcggcgc tgcgtggatc
 aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcattt ggagggcgag
 ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct

ccttatgggtg	actccccggt	aagcacaatc	ccactttgtg	atgagacctc	tgtcgagtgt	780
agaatacagt	cactgactcc	acttcgtcca	gctgagcgag	gaggttgcaa	gtgcaattgc	840
ggaactcctc	cccgtatggg	ctcagctgat	cgaagagtat	agccttgaag	acccccaggc	900
gagccctcag	gcgaagcggc	tcgacagtgt	gagcttcgag	cactactgtg	agaaggacct	960
aaacttgctt	gctgtttctc	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcgggtgtgga	1020
agccccagag	atcagcatgc	tttttctcac	cgactacatc	aagagtgcc	ccgggtctcag	1080
taatattgtc	tcggacaaga	aagacggcgg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140
cggtgtcctc	tcaggtaggg	gactcgtttc	ttagtggtca	ttccaggtat	gcagtcgatt	1200
tgccatgcc	tgtcaaagga	acttgttcca	ggctcagtc	acctcaacac	ccccgtcgt	1260
ggaattgagc	agtccggctc	cggctgtata	gtacgatcgg	cctcggggcg	cgtgttcgga	1320
agcaaaaagg	tggtggtttc	gttaccgaca	acattgtatc	ccaccttgac	attttccacca	1380
cctcttcccg	ccgagaagca	agcattggcg	gaaaaatcta	tcctcggcta	ctatagcaag	1440
atagtcttcg	tatgggacaa	cccgtgggtg	cgcgaaacaag	gcttctcggg	cgtcctccaa	1500
tcgagctgtg	accccatctc	atttgccaga	gataccagca	tcgaagtcca	tcggcaatgg	1560
tcctattacct	gtttcatggt	cggagaccgg	ggacgggaagt	ggccccaca	gtccaagcag	1620
gtacgacaaa	agtctgtctg	ggaccaactc	cgcgcagcct	acgagaacgc	cgggggcccc	1680
gtcccagagc	cggccaaagt	gtcgaatac	gagtggtcca	agcagcagta	tttccaagga	1740
gctccgagcg	ccgtctatgg	gctgaacgat	ctcatcaaac	tgggttcggc	gctcagaacg	1800
ccgttcaagt	gtgttcattt	cgttggaacg	gagacgtctt	tagtttggaa	aggggtatatg	1860
gaaggggcca	tacgatcggg	tcaacgaggt	gctgcagaag	ttgtggctag	cctggtgcc	1920
gcagcatag						1929

<210> 38

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 38

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
1				5				10					15		
Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70				75					80	
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85					90						95	
Leu	Lys	Ser	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
		115					120					125			
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135						140			
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155				160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165					170					175		
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
			180					185					190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
		195					200					205			
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
	210					215					220				
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
225					230				235					240	

<221> misc_feature
 <222> (648)...(648)
 <223> n = A,T,C or G

<400> 39
 atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc aggggtattct 60
 cacgtcggcg taggcccaga cggagggagg tatgtgacaa tagctggaca gattggacaa 120
 gacgcttcgg gcgtgacaga ccctgcctac gagaacacagg ttgcccgaagc attcgccaat 180
 ctgcgagctt gccttgctgc agttggagcc acttcaaacg acgtcaccaa gctcaattac 240
 tacatcgteg actaagcccc gagcaaaactc accgcaattg gagatgggct gaaggctacc 300
 tttgcccctg acaggtctcc tccttgcaag ctgggtgccag tgtcggcctt gtcttcacct 360
 gaatacctct ttgaggttga tgccacggcg ctgggtgcggg gacacacgac cccagacaac 420
 gttgcggagc tggtagtggg gggcgctggc ttgagcgggt tggagacggc acgcaaagtc 480
 caggccgcgc gtctgtctct cctcgttctt gagggcgatgg atcgtgtagg gggaaagact 540
 ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600
 aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcatnt ggagggcgag 660
 ctccagagga cgactggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720
 ccttatgggt actccttggg aagcacaatc ccactttgtg atgagacctc tgcagagtgt 780
 agaatacagt cactgattcc acttcgtcca gctgagcgag gaggttgcaa gtgcaattgc 840
 ggaactctc cccgtatggg ctcagctgat cgaagagcat agccttcaag acctcaaggc 900
 gagccctcag gcgaagcggc tcgacagtgt gagcttcggc cactactgtg agaaggaaat 960
 aaacttgccg gctgttctcg gcgtagcaaa ccagatcaca cgcgctctgc tcgggtgtgga 1020
 agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgcc aagggtctcag 1080
 taatatcttc tgggacaaga aagacggcgg gcagtatatg cgatgcaaaa cagggtcgtg 1140
 tgggtgtcgc tcagggtggg gactcgtttc tcaagtgggc atttcaggta tgcagtcgat 1200
 ttgccatgcc atgtcaaaag aacttgttcc aggtcagtg caccacaaca ccccgctgc 1260
 tgaaattgag cagtcggcat ccggctgtac agtaagatcg gcctcgggcg ccgtgttcgc 1320
 aagcaaaaag gtgggtggtt cgttacccgac aaccttgat cccaccttga catcttcacc 1380
 acctctcccc gccgagaagc aagcattggc ggaaaattct atcctgggct actatagcaa 1440
 gatagtcttc gtatgggaca agccgtgggt gcgcgaacaa ggcttctcgg gcgtctctca 1500
 atcgagctgt gaccccatct catctgccag agataccagc atcgacgtcg atcgacaatg 1560
 gtccattacc tgtttcatgg tcggagaccc gggacggaag tggteccaac agtccaagca 1620
 ggtacgacaa aagtctgtct gggaccaact ccgcgcagcc tacgagaacg ccggggccca 1680
 agtcccagag ccggccaacg tgctcgaaat cgagtggtcg aagcagcagt atttccaagg 1740
 agtcccgagc gccgtctatg ggctgaacga tctcatcaca ctgggttcgg cgtcagaac 1800
 gccgttcaag agtgttcatt tcgttggaaac ggagacgtct ttagtttgga aagggtatat 1860
 ggaagggggc atacgatcgg gtcaacgagg tgcctgcagaa gttgtggcta gcctgggtgc 1920
 agcagcatag 1930

<210> 40
 <211> 598
 <212> PRT
 <213> *Exophiala spinifera*

<220>
 <221> VARIANT
 <222> (216)...(216)
 <223> Xaa = Any Amino Acid

<400> 40
 Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1 5 10 15
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys

50	55	60
Leu Ala Ala Val Gly	Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65	70	75
Tyr Ile Val Asp Tyr	Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	80
	85	90
Leu Lys Ala Thr Phe	Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	95
	100	105
Pro Val Ser Ala Leu	Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	110
	115	120
Thr Ala Leu Val Pro	Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	125
	130	135
Val Val Gly Ala Gly	Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln	140
145	150	155
Ala Ala Gly Leu Ser	Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly	160
	165	170
Gly Lys Thr Leu Ser	Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn	175
	180	185
Asp Leu Gly Ala Ala	Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser	190
	195	200
Arg Leu Phe Glu Arg	Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr	205
	210	215
Gly Asn Ser Ile His	Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro	220
225	230	235
Tyr Gly Asp Ser Leu	Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu	240
	245	250
Leu Leu Pro Val Trp	Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp	255
	260	265
Leu Lys Ala Ser Pro	Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala	270
	275	280
His Tyr Cys Glu Lys	Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn	285
	290	295
Gln Ile Thr Arg Ala	Leu Leu Gly Val Glu Ala His Glu Ile Ser Met	300
305	310	315
Leu Phe Leu Thr Asp	Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile	320
	325	330
Phe Ser Asp Lys Lys	Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly	335
	340	345
Met Gln Ser Ile Cys	His Ala Met Ser Lys Glu Leu Val Pro Gly Ser	350
	355	360
Val His Leu Asn Thr	Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly	365
	370	375
Cys Thr Val Arg Ser	Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val	380
385	390	395
Val Val Ser Leu Pro	Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro	400
	405	410
Pro Leu Pro Ala Glu	Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly	415
	420	425
Tyr Tyr Ser Lys Ile	Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu	430
	435	440
Gln Gly Phe Ser Gly	Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe	445
	450	455
Ala Arg Asp Thr Ser	Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys	460
465	470	475
Phe Met Val Gly Asp	Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln	480
	485	490
Val Arg Gln Lys Ser	Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn	495
	500	505
Ala Gly Ala Gln Val	Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp	510

515	520	525
Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu		
530	535	540
Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser		
545	550	555
Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met		
565	570	575
Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala		
580	585	590
Ser Leu Val Pro Ala Ala		
595		

<210> 41
 <211> 1928
 <212> DNA
 <213> Rhinocladiella atrovirens

<220>
 <221> intron
 <222> (739)...(811)
 <221> intron
 <222> (1134)...(1185)

<400> 41

atggcacttg	caccgagcta	catcaatccc	ccaaaacctcg	cctccccagc	agggtattcc	60
cacgtcggcg	taggccc aaa	cggaggggagg	tatgogacaa	tagctggaca	gattggacaa	120
gacgttcggg	ccgtgacaga	ccctgcctac	gagaaacagg	ttgccc aagc	attcgccaac	180
ctgcgagctt	gtcttgctgc	agttggagcc	acttcaaacg	acattaccaa	gtcgaattac	240
tacatcgctg	actacaaccc	gagcaaactc	acgcgaattg	gagatgggct	gaaggctacc	300
tttgcccttg	acaggctccc	tccttgcaag	ctgggtgccag	tgccggccct	ggcttcacct	360
gaataccctt	ttgaggttga	tgccacggcg	ctgggtccag	gacactcaac	cccagacaat	420
gttgcggaag	tggtcgtggt	gggcgctggc	ttgagcgggt	tggagacggc	acgcaaagtc	480
caggctgccc	ggctgtcctg	cctcgcttct	gaggcgatgg	atcgtgtggg	gggaaagact	540
ctgagcgtac	aatcgggtcc	cggcaggagc	gtatcaaatg	acctcggcgc	tgcgtggatc	600
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acgggtacaac	cactacagct	720
cettatgggt	attccctggg	aagcacaatt	ccatcttggt	atgagacctc	tgtcgtgtgt	780
agaatacagt	cgtgactcc	acatcgctca	gtgagcgag	gaggttgcaa	gtgcaactgc	840
ggaactcctt	cccgcattgg	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaagcagc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct	960
aagcttgcc	gctgttctcg	gctgtggcaa	ccagatcaca	cgcgctctgc	tccgtgtgga	1020
agcccacgag	atcagcatgc	ttttctctac	cgaactacat	aagagtgcga	ccggtctcag	1080
taatatgtgc	tcggataaga	aagacgggtg	gcagtatatg	cgatgcaaaa	caggtgctgt	1140
tggtgttctc	tcagtgggag	actcgtttct	tagtggctcat	tccaggtatg	cagtcgcttt	1200
gccatgccat	gtcaaaaggaa	cttggtccag	gtcagtgca	cctcaacacc	cccgctgcgc	1260
aaattgagca	gtcggcatcc	ggctgtacag	tacgatcggc	ctcggggcggc	gtgttcggaa	1320
gtaaaaaggt	ggtgggttcg	ttaccgacaa	ccttggtatcc	caccttgata	ttttcaccac	1380
ctcttccgcg	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ccgtgggtgg	gogaacaagg	cttctcgggc	gtcctccaat	1500
cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggcaatggt	1560
ccattacctg	tttcatgggc	ggagaccggg	gaagggaagt	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcgcagccta	cgagaacgcc	ggggcccaag	1680
tcccagagcc	ggccaaggtg	ctcgagatgc	agtggtcgaa	gcagcagtat	ttccaaggag	1740
cgcgcagcgt	cgtctatggg	ctgaactgtc	tcaaacactc	gggttcggcg	ctcagaacgc	1800
cgttcaagg	gttctaatte	gttgggaacg	agaagctttt	ggtttggaag	gggtatattg	1860
aaggggccat	acgatcgggt	cagcgaggcg	ctgcagaagt	tgtggctagc	ctgggtgccag	1920
cagcatag						1928

<210> 42
 <211> 598
 <212> PRT
 <213> Rhinocladiella atrovirens

<400> 42
 Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
 1 5 10 15
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Ala
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
 130 135 140
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile
 180 185 190
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205
 Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
 210 215 220
 Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr
 225 230 235 240
 Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu
 245 250 255
 Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro
 260 265 270
 Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His
 275 280 285
 Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn
 290 295 300
 Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
 305 310 315 320
 Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
 325 330 335
 Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
 340 345 350
 Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
 355 360 365
 Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
 370 375 380
 Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val
 385 390 395 400
 Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro

				405						410					415				
Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Lys	Ser	Ile	Leu	Gly				
			420					425					430						
Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu				
		435					440					445							
Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe				
	450					455					460								
Ala	Arg	Asp	Thr	Ser	Ile	Glu	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys				
465					470					475					480				
Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln				
				485					490					495					
Val	Arg	Gln	Lys	Ser	Val	Trp	Asn	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn				
			500					505					510						
Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp				
		515					520					525							
Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Val	Val	Tyr	Gly	Leu				
	530					535					540								
Asn	Cys	Leu	Asn	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Gly				
545					550					555					560				
Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met				
				565					570					575					
Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala				
			580					585					590						
Ser	Leu	Val	Pro	Ala	Ala														
			595																

<210> 43
 <211> 1928
 <212> DNA
 <213> *Rhinocycladiella atrovirens*

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
 <222> (1134)...(1186)

<400> 43																			
atggcacttg	caccgagcta	catcaatccc	ccaaacctcg	cctccccagc	agggtattcc														60
tacgtcggcg	taggccc aaa	cggaggagg	tatgtgacaa	tagctggaca	gattggacaa														120
gacgcttcgg	cgtgacaga	ccctgcctac	gagaaacagg	ttgcccagc	attcgccaac														180
ctgcgagctt	gtcttgctgc	agttggagcc	acttcaaaacg	acattaccaa	gtccaattac														240
tacatcgctg	actacaaccc	gagcaaacctc	accgcaattg	gagatgggct	gaaggctacc														300
tttgcccttg	acaggctccc	tccttgcaag	ctgggtgccag	tgcgggccct	ggettcacct														360
gaataacctt	ttgaggttga	tgccacggcg	ctgggtccag	gacactcaac	cccagacaat														420
gttgcggaag	tggtcgtggt	gggcgctggc	ttgagcggtt	tggagacggc	acgcaaaagtc														480
caggctgcag	ggctgtccctg	cctcgttctt	gaggcgatgg	atcgtgtggg	gggaaagact														540
ctgagcgtac	aatcgggtcc	cggcaggacg	actatcaatg	acctcggcgc	tgcgtggatc														600
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag														660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct														720
ccttatgggtg	attccctggt	aagcacaatt	ccatcttggtg	atgagacctc	tgtcgtgtgt														780
agaatacagt	cgtgactcc	acatcgctcc	gctgagcgag	gaggttgcaa	gtgcactcgc														840
ggaactcctt	cccgcctggt	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc														900
gagccctcaa	gcgaagcagc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct														960
aaacttgctt	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tgggtgtgga														1020
agcccacgag	atcagcatgt	tttttctcac	cgaactacatc	aagagtgcc	ccggtctcag														1080
taatattgtc	tcggataaga	aagacgggtg	gcagttatatg	cgatgcaaaa	caggtgcgtg														1140

tggtgtttctc	tcagtgggag	actcgtttct	tagtggtcat	tcaggtatg	cagtcgcttt	1200
gccatgccat	gtcaaaggaa	cttggtccag	gtcagtgca	cctcaacacc	ccgtcgcgc	1260
aaattgagca	gtcggcatcc	ggctgtacag	tacgatcggc	ctcggggcgc	gtgttccgaa	1320
gtaaaaaggt	ggtggtttcg	ttaccgacaa	ccttgatcc	caccttgata	ttttcaccac	1380
ctcttccgc	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ccgtggtggc	gcgaacaagg	cttctcgggc	gtctctccat	1500
cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggaatggg	1560
ccattacctg	tttcatgggc	ggagaccgg	gacggaagt	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcgcagccta	cgagaacgcc	ggggcccaag	1680
tcccagagcc	ggccaacgtg	ctcgagatcg	agtgggtcgaa	gcagcagtat	ttccaaggag	1740
cgcgagcgc	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaaggg	tggtcatttc	gttggaaagg	agacgtcttt	gggttggaag	gggtatatgg	1860
aaggggccat	acgatcgggt	cagcgaggcg	ctgcagaagt	tgtggctagc	ctggtgccag	1920
cagcatag						1928

<210> 44

<211> 591

<212> PRT

<213> *Rhinocycladiella atrovirens*

<400> 44

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Leu	Ala	Ser	Pro
1				5				10						15	
Ala	Gly	Tyr	Ser	Tyr	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr
65					70				75					80	
Tyr	Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85					90						95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
			115				120					125			
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135					140				
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155				160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165					170					175		
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Gly	Arg	Thr	Thr	Ile	Asn
			180					185					190		
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Lys
	195					200					205				
Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly
	210				215						220				
Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr
225				230					235					240	
Gly	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu
			245					250					255		
Pro	Ala	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Glu	Asp	Pro	Lys	Ala
			260					265					270		
Ser	Pro	Gln	Ala	Lys	Gln	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys
	275					280						285			
Glu	Lys	Leu	Asn	Leu	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg

290		295		300											
Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Phe	Phe	Leu	Thr
305					310					315					320
Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Val	Ser	Asp	Lys
			325						330					335	
Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Leu
		340						345					350		
Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn
	355					360					365				
Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg
	370					375					380				
Ser	Ala	Ser	Gly	Gly	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Leu	Pro	Thr
385					390				395					400	
Leu	Tyr	Pro	Thr	Leu	Ile	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
			405					410						415	
Ala	Leu	Ala	Glu	Lys	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
		420						425					430		
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
	435					440					445				
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Glu
	450					455					460				
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
465					470				475					480	
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
			485					490						495	
Asn	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
		500						505					510		
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
	515						520					525			
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Cys	Leu	Asn	Thr	Leu	Gly
	530					535					540				
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Gly	Val	His	Phe	Val	Gly	Thr	Glu
545					550				555					560	
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
			565					570					575		
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
		580					585						590		

<210> 45
 <211> 1928
 <212> DNA
 <213> *Rhinocycladiella atrovirens*

<220>
 <221> intron
 <222> (739)... (811)

<221> intron
 <222> (1134)... (1185)

<400> 45	
atggcacttg	cacgageta catcaatccc ccaaactcgc cctccccagc aggggtattcc 60
cacgtcggcg	taggccc aaa cggagggagg tatgtgacaa tagctggaca gattggacaa 120
gacgtttcgg	ccgtgacaga cctgcctac gagaaacagg ttgcccagc attogccaac 180
ctgcgagctt	gttttgcctgc agttggagcc acttcaaacg acattaccaa gctcaattac 240
tacatcgtcg	actacaaccc gagcaaactc accgaattg gagatgggct gaaggctacc 300
tttgcccttg	acaggtctccc tctttgcaag ctgggtgcag tgccggccct ggtttcacct 360
gaatacctct	ttgaggttga tgctacggcg ctgggttcag gacactcaac cccagacaat 420

gttgccgacg	tggtcgtggt	gggcgctggc	ttgagcgggt	tggagacggc	acgcaaagtc	480
caggctgccg	ggctgtcctg	cctcgttctt	gaggcgatgg	atcgtgtggg	gggaaagact	540
ctgagcgtac	aatcgggtcc	cggcaggacg	actatcaatg	acctcggcgc	tgcgtggatc	600
aatgacagca	accaaaagcg	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatgggt	attccctggt	aggcacaatt	ccatcttggt	atgagacctc	tgctcgtgtg	780
agaatacagt	cgctgactcc	acatcgctcc	gctgagcgag	gaggttgcaa	gtgcactcgc	840
ggaactcctt	cccgcattgt	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaagcagc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct	960
aaacttgcc	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agcccacgag	atcagcatgc	ttttctcac	cgactacatc	aagagtgcga	ccggtctcag	1080
taatattgtc	tcggataaga	aagacggtgg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140
tggtgttctc	tcagtgaggag	actcgtttct	tagtggtcat	tcaggtatg	cagtcgcttt	1200
gccatgccat	gtcaaaggaa	cttgttccag	gctcagtgc	cctcaacacc	cccgctcgccg	1260
aaattgagca	gtcggcatcc	ggctgtacag	taagatcggc	ctcgggcggc	gtgttccgaa	1320
gtaaaaaggt	ggtggtttcg	ttaccgacaa	ccttggtatcc	caccttgata	ttttcaccac	1380
ctcttccgcg	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttcgt	atgggacaa	ctgtggtggc	gcgaacaagg	cttctcgggc	gtctctcaat	1500
cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggcaatggt	1560
ccattacctg	tttcatggtc	ggagaccggg	gaagggaagt	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcgcagccta	cgagaacgcc	ggggcccaag	1680
tcccagagcc	ggccaacgtg	ctcgagatcg	agtggtcgaa	gcagcagtat	ttccaaggag	1740
cgccgagcgc	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaaggg	tggttcatttc	gttggaacgg	agaagctctt	ggtttgaaa	gggtatatgg	1860
aaggggccat	acgatcgggt	cagcgaggcg	ctgcagaagt	tgtgcctagc	ctggtgccag	1920
cagcatag						1928

<210> 46

<211> 591

<212> PRT

<213> *Rhinocladiella atrovirens*

<400> 46

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Ala	Ser	Pro	Ala
1				5				10					15		
Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Val	Thr
			20					25					30		
Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro	Ala
		35					40					45			
Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys	Leu
	50					55				60					
Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr	Tyr
65					70				75					80	
Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	Leu
			85					90					95		
Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	Pro
			100					105					110		
Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala	Thr
		115					120					125			
Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	Val
		130					135					140			
Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
145					150				155					160	
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
			165					170					175		
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
			180					185					190		
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Phe

Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	Gly	Gly	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70					75					80
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
				85					90					95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
			100					105					110		
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
		115					120					125			
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135					140				
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155					160
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165						170					175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
			180					185					190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
		195					200					205			
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
	210					215					220				
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
225					230					235					240
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala
			245						250					255	
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln
		260						265					270		
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe
		275					280					285			
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val
	290					295					300				
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile
305					310					315					320
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser
			325						330					335	
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys
		340						345					350		
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro
	355						360					365			
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala
	370					375					380				
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys
385					390					395					400
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe
			405						410					415	
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile
			420					425					430		
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp
	435						440					445			
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile
	450					455					460				
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile
465					470					475					480

Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser
			485					490					495		
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr
			500					505					510		
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile
		515					520					525			
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr
	530					535					540				
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe
545					550					555					560
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly
			565					570						575	
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val
			580					585					590		
Val	Ala	Ser	Leu	Val	Pro	Ala	Ala								
		595				600									

<210> 48

<211> 1392

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteine 461

<400> 48

aaa	gac	aac	gtt	gcg	gac	gtg	gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggc	48
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	
1				5					10				15			
ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggc	ctg	tcc	tgc	ctc	gtt	96
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	
			20				25					30				
ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tgc	144
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	
			35				40					45				
ggc	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	192
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	
	50					55				60						
gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	240
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	
	65				70				75				80			
gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	288
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	
			85					90					95			
gac	ggc	aca	acc	act	aca	gct	cct	tat	ggc	gac	tcc	ttg	ctg	agc	gag	336
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
			100					105				110				
gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	384

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *	
450 455 460	

<210> 49
 <211> 463
 <212> PRT
 <213> Unknown

<220>
 <223> Cys (-) APAO; removal of cysteine 461

<400> 49

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	

145		150		155		160									
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
		165				170								175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
		180						185						190	
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
		195					200						205		
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
	210					215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235				240	
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
				245					250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
		260						265						270	
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
	275						280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
290					295						300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315				320	
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
			325						330					335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
		340						345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
	355						360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
370					375					380					
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385			390						395					400	
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
		405						410						415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
		420						425					430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
	435					440						445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
450					455						460				

<210> 50
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 50	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	

20	25	30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 35 40 45			144
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 50 55 60			192
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 65 70 75 80			240
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85 90 95			288
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 100 105 110			336
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115 120 125			384
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 130 135 140			432
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145 150 155 160			480
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175			528
ggc gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190			576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205			624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala 210 215 220			672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240			720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255			768

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tgc tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270	816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285	864
gca ttg gcg gaa aat tct atc ctg gcc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300	912
gta tgg gac aag ccg tgg tgg cgc gaa caa gcc ttc tgc gcc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320	960
caa tgc agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350	1056
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385 390 395 400	1200
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405 410 415	1248
tgc gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 420 425 430	1296
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgc ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 435 440 445	1344
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala * 450 455 460	1392

<210> 51
 <211> 463
 <212> PRT
 <213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51

Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
1				5					10					15	
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Gly	Leu	Ser	Cys	Leu	Val	
			20					25				30			
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser
		35					40				45				
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn
50						55				60					
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
65					70				75					80	
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
				85				90					95		
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu
			100					105				110			
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115					120					125			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
130						135				140					
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155				160	
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
				165					170					175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180					185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
		195					200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Ser	His	Ala
210						215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230						235			240	
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
				245					250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
			260					265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
		275					280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
290						295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315				320	
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
				325					330					335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
			340					345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
		355					360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
370						375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385					390						395			400	
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
				405					410					415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
			420					425					430		

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 52
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 169, 359, and
 461

<400> 52
 aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15
 ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctc gtt 96
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
 20 25 30
 ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95
 gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag 336
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110
 gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg 384
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125
 atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag 432
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140
 cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac 480
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggc gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	

385	390	395	400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt				1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag				1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt				1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	435	440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag				1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *	450	455	460	

<210> 53
 <211> 463
 <212> PRT
 <213> Unknown

<220>
 <223> Cys (-) APAO; removal of cysteines 169, 359, and
 461

<400> 53

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly				
1	5	10	15	
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val				
20	25	30		
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser				
35	40	45		
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn				
50	55	60		
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu				
65	70	75	80	
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln				
85	90	95		
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu				
100	105	110		
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu				
115	120	125		
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys				
130	135	140		
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn				
145	150	155	160	
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu				
165	170	175		
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile				
180	185	190		
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly				
195	200	205		
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala				
210	215	220		
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val				

